

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claim 1. (Previously presented) A method for altering fiber development or properties of a fiber-producing plant comprising the step of providing cells of said plants a plant with a chimeric gene comprising the following operably linked DNA fragments:

a plant expressible promoter;
a the coding region from a plant sucrose synthase gene; and
a transcription termination and polyadenylation signal which functions in said plant cells.

Claim 2. (Currently amended) The method according to claim 1, wherein said coding region from a plant sucrose synthase gene is translated into an active plant sucrose synthase protein ~~gene is at least 95% homologous to a DNA selected from the group consisting of the DNA of SEQ ID NO: 1 and DNA with GenBank accession number BM094593 (*Glycine max*); BM093753 (*Glycine max*); BM093158 (*Glycine max*); BM092695 (*Glycine max*); BM092443 (*Glycine max*); BM092322 (*Glycine max*); BM085310 (*Glycine max*); BM085020 (*Glycine max*); AY059416 (*Zea mays*); AF273253 (*Beta vulgaris*); L39940 (*Oryza sativa*); AJ316590 (*Nostoc punctiforme*); AJ316589 (*Nostoc punctiforme*); AJ316596 (*Anabaena sp.*); AJ316595 (*Anabaena sp.*); AJ316584 (*Anabaena sp.*); BM005654 (*Crocus sativus*); BI973032 (*Glycine*~~

~~max); BI971794 (Glycine max); AF367450 (Prunus persica); BI945506 (Glycine max); BI944973 (Glycine max); AF420224 (Carica papaya); BI788449 (Glycine max); BI788359 (Glycine max); BI787127 (Glycine max); BI787033 (Glycine max); BI787000 (Glycine max); BI786823 (Glycine max); BI784933 (Glycine max); BI784627 (Glycine max); BI700214 (Glycine max); BI699934 (Glycine max); BI699923 (Glycine max); BI699585 (Glycine max); BI543240 (Sugar beet); BI498340 (Glycine max); BI471463 (Glycine max); BI427241 (Glycine max); BI427174 (Glycine max); BI427022 (Glycine max); BI426915 (Glycine max); AF393809 (Apium graveolens); BI321173 (Glycine max); BI320832 (Glycine max); BI316894 (Glycine max); BI316826 (Glycine max); BI316405 (Glycine max); BI315949 (Glycine max); BI203222 (Lycopersicon esculentum); BI176503 (Solanum tuberosum); BG273882 (Grape berries); AY034958 (Arabidopsis thaliana); AF378187 (Oryza sativa); BG790580 (Glycine max); BG790079 (Glycine max); BG726150 (Glycine max); BG654021 (Glycine max); BG653916 (Glycine max); BG653624 (Glycine max); BG652711 (Glycine max); BG652507 (Glycine max); BG649914 (Glycine max); BG649831 (Glycine max); AJ309093 (Pinus pinaster); BG507656 (Glycine max); BG405632 (Glycine max); BG405474 (Glycine max); BG405204 (Glycine max); BG405017 (Glycine max); BG363730 (Glycine max); BG362638 (Glycine max); BG359764 (Glycine max); BG359452 (Glycine max); BG359307 (Glycine max); AJ311496 (Pisum sativum); BG239317 (Glycine max); BG237287 (Glycine max); BG157592 (Glycine max); BG155900 (Glycine max); BG047402 (Glycine max); BG046717 (Glycine max); BG046686 (Glycine max); BG046043 (Glycine max); BG043243 (Glycine max); BG042159 (Glycine max); BG041814 (Glycine max); AB045710 (Pyrus pyrifolia); BF597682 (Glycine max); BF597330 (Glycine max);~~

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~~*sativum*); AJ131964 (*Medicago truncatula*); AJ131943 (*Medicago truncatula*);~~
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~~AI441989 (*Glycine max*); AI441004 (*Glycine max*); AI437923 (*Glycine max*);~~
~~AI437907 (*Glycine max*); AI437840 (*Glycine max*); AJ010639 (*Anabaena* sp.);~~
~~AJ011535 (*Lycopersicon esculentum*); D10266 (*Vigna radiata*); L03366 (*Oryza*~~

~~sativa~~); AF030231 (~~Glycine max~~); M97551 (~~Vicia faba~~); AJ000153 (~~Triticum aestivum~~); AF079523 (~~Musa acuminata~~); AF079851 (~~Pisum sativum~~); AJ001071 (~~Pisum sativum~~); AF049487 (~~Medicago sativa~~); AF054446 (~~Mesembryanthemum crystallinum~~); AA753339 (~~Oryza sativa~~); AA752298 (~~Oryza sativa~~); AA752293 (~~Oryza sativa~~); AA753445 (~~Oryza sativa~~); AA753437 (~~Oryza sativa~~); AA753297 (~~Oryza sativa~~); AA752123 (~~Oryza sativa~~); AA751990 (~~Oryza sativa~~); AA750692 (~~Oryza sativa~~); AA750079 (~~Oryza sativa~~); AA749692 (~~Oryza sativa~~); AA749554 (~~Oryza sativa~~); AA720478 (~~Mesembryanthemum crystallinum~~); AA661050 (~~Medicago truncatula~~); AA661041 (~~Medicago truncatula~~); AA660686 (~~Medicago truncatula~~); D88412 (~~Cotton~~); D10418 (~~Rice~~); D21308 (~~Rice~~); D29733 (~~Rice~~); X81974 (~~B. vulgaris~~); X92378 (~~A. glutinosa~~); Z56278 (~~V. faba~~); Z48640 (~~V. faba~~); X98598 (~~P. sativum~~); T25261 (~~Zea mays~~); T23326 (~~Zea mays~~); T14713 (~~Zea mays~~); T14662 (~~Zea mays~~); T14661 (~~Zea mays~~); X75332 (~~D. carota~~); X02382 (~~Zea mays~~); X02400 (~~Zea mays~~); X70990 (~~A. thaliana~~); X60987 (~~A. thaliana~~); X69773 (~~V. faba~~); X73477 (~~S. tuberosum~~); Z11532 (~~S. officinarum~~); Z15028 (~~O. sativa~~); X64770 (~~O. sativa~~); X59046 (~~O. sativa~~); X66728 (~~H. vulgare~~); X65871 (~~H. vulgare~~); X69931 (~~H. vulgare~~); A27685 (~~O. sativa~~); W21612 (~~Zea mays~~); U24088 (~~Solanum tuberosum~~); U24087 (~~Solanum tuberosum~~); X73221 (~~H. vulgare~~); L32898 (~~Zea mays~~); F13913 (~~Arabidopsis thaliana~~); F13912 (~~Arabidopsis thaliana~~); U21129 (~~Solanum tuberosum~~); M26672 (~~Triticum aestivum~~); M26671 (~~Triticum aestivum~~); L19762 (~~Lycopersicon esculentum~~); M18745 (~~Potato~~); L33244 (~~Zea mays~~); L22296 (~~Zea mays~~); and Z17959 (~~Arabidopsis thaliana~~).

Claim 3. (Currently amended) The method according to claim 1, wherein said coding region from a plant sucrose synthase gene comprises a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID NO 2.

Claim 4. (Withdrawn; currently amended) The method according to claim 1, wherein said ~~RNA is capable of reducing~~ coding region from a plant sucrose synthase gene reduces the expression of an endogenous sucrose synthase gene.

Claim 5. (Withdrawn) The method according to claim 4, wherein said coding region comprises a nucleotide sequence selected from the group consisting of

a nucleotide sequence comprising at least 19 or 25 contiguous nucleotides having at least 70% sequence identity to a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID NO 2 or the complement thereof; and

a nucleotide sequence comprising at least 25 contiguous nucleotides having at least 70% sequence identity to a nucleotide sequence encoding a polypeptide comprising the nucleotide sequence of SEQ ID No 1 or the complement thereof.

Claim 6. (Withdrawn) The method according to claim 5, wherein said coding region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 2208 to the nucleotide at position 2598 or the complement thereof.

Claim 7. (Withdrawn) The method according to claim 5, wherein said coding region comprises both sense and antisense nucleotide sequences capable of forming a double stranded RNA molecule.

Claim 8. (Previously presented) The method according to any one of claims 1, 2, or 3, wherein said promoter is a subterranean clover stunt virus promoter.

Claim 9. (Previously presented) The method according to any one of claims 1, 2, or 3, wherein said fiber-producing plant is a cotton plant.

Claim 10. (Original) The method according to claim 8, wherein said fiber-producing plant is a cotton plant.

Claim 11. (Deleted)

Claim 12. (Currently amended) A method for improving fiber yield in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments

a plant expressible promoter;

the coding region from a a sucrose synthase gene; and

a transcription termination and polyadenylation signal which functions

in said plant cells.

Claim 13. (Previously presented) A method for improving fiber quality in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments

a plant expressible promoter;

the coding region from a sucrose synthase gene; and

a transcription termination and polyadenylation signal which functions in said plant cells.

Claim 14. (Previously presented) A method for increasing seed size in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments:

a seed-specific promoter;

the coding region from a sucrose synthase gene ; and

a transcription termination and polyadenylation signal which functions in said plant cells.

Claim 15. (Previously presented) A fiber-producing plant comprising in its genome a chimeric DNA comprising the following operably linked DNA fragments:

a plant expressible promoter;

the coding region from a sucrose synthase gene; and

a transcription termination and polyadenylation signal which functions in said plant.

Claim 16. (Currently amended) A fiber-producing plant according to claim 15, wherein said coding region from a plant sucrose synthase gene is translated into an active plant sucrose synthase protein is at least 95% homologous to a DNA selected from the group consisting of the DNA of SEQ ID NO: 1; DNA with GenBank accession number ~~BM094593 (*Glycine max*); BM093753 (*Glycine max*); BM093158 (*Glycine max*); BM092695 (*Glycine max*); BM092443 (*Glycine max*); BM092322 (*Glycine max*); BM085310 (*Glycine max*); BM085020 (*Glycine max*); AY059416 (*Zea mays*); AF273253 (*Beta vulgaris*); L39940 (*Oryza sativa*); AJ316590 (*Nostoc punctiforme*); AJ316589 (*Nostoc punctiforme*); AJ316596 (*Anabaena sp.*); AJ316595 (*Anabaena sp.*); AJ316584 (*Anabaena sp.*); BM005654 (*Crocus sativus*); BI973032 (*Glycine max*); BI971794 (*Glycine max*); AF367450 (*Prunus persica*); BI945506 (*Glycine max*); BI944973 (*Glycine max*); AF420224 (*Carica papaya*); BI788449 (*Glycine max*); BI788359 (*Glycine max*); BI787127 (*Glycine max*); BI787033 (*Glycine max*); BI787000 (*Glycine max*); BI786823 (*Glycine max*); BI784933 (*Glycine max*); BI784627 (*Glycine max*); BI700214 (*Glycine max*); BI699934 (*Glycine max*); BI699923 (*Glycine max*); BI699585 (*Glycine max*); BI543240 (*Sugar beet*); BI498340 (*Glycine max*); BI471463 (*Glycine max*); BI427241 (*Glycine max*); BI427174 (*Glycine max*); BI427022 (*Glycine max*); BI426915 (*Glycine max*); AF393809 (*Apium graveolens*); BI321173 (*Glycine max*); BI320832 (*Glycine max*); BI316894 (*Glycine max*); BI316826 (*Glycine max*); BI316405 (*Glycine max*); BI315949 (*Glycine max*); BI203222 (*Lycopersicon esculentum*); BI176503 (*Solanum tuberosum*); BG273882 (*Grape berries*); AY034958 (*Arabidopsis thaliana*); AF378187 (*Oryza sativa*); BG790580 (*Glycine max*); BG790079 (*Glycine max*); BG726150 (*Glycine max*); BG654021 (*Glycine max*); BG653916 (*Glycine max*);~~

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~~max~~; AW307001 (~~Glycine max~~); AW306834 (~~Glycine max~~); AB018561 (~~Citrullus lanatus~~); AB029401 (~~Citrus unshiu~~); AB022092 (~~Citrus unshiu~~); AB022091 (~~Citrus unshiu~~); AW279073 (~~Glycine max~~); AW279053 (~~Glycine max~~); AW278487 (~~Glycine max~~); AJ388994 (~~Medicago truncatula~~); AJ388888 (~~Medicago truncatula~~); AW234887 (~~Glycine max~~); AJ238219 (~~Triticum aestivum~~); AJ238218 (~~Triticum aestivum~~); AJ238217 (~~Triticum speltoides~~); AW201670 (~~Glycine max~~); AW185801 (~~Glycine max~~); AW185627 (~~Glycine max~~); AJ249624 (~~Triticum aestivum~~); AJ249623 (~~Triticum aestivum~~); AW164630 (~~Glycine max~~); AW164393 (~~Glycine max~~); AW133248 (~~Glycine max~~); AW101578 (~~Glycine max~~); AW100191 (~~Glycine max~~); AW100069 (~~Glycine max~~); AW099557 (~~Glycine max~~); X96938 (~~T. gesneriana~~); X96939 (~~T. gesneriana~~); AW035186 (~~Lycopersicon esculentum~~); AW033439 (~~Lycopersicon esculentum~~); AW032339 (~~Lycopersicon esculentum~~); AJ132002 (~~Craterostigma plantagineum~~); AJ132001 (~~Craterostigma plantagineum~~); AJ132000 (~~Craterostigma plantagineum~~); AJ131999 (~~Craterostigma plantagineum~~); AI973811 (~~Glycine max~~); AI973710 (~~Glycine max~~); AI973540 (~~Glycine max~~); AI967739 (~~Lotus japonicus~~); AI965972 (~~Glycine max~~); AI960742 (~~Glycine max~~); AI960703 (~~Glycine max~~); AI930917 (~~Glycine max~~); AI900130 (~~Glycine max~~); AI900087 (~~Glycine max~~); AI855470 (~~Glycine max~~); AA080634 (~~Saccharum sp.~~); AA080610 (~~Saccharum sp.~~); AA269294 (~~Saccharum sp.~~); AA080580 (~~Saccharum sp.~~); AI736370 (~~Glycine max~~); AI731292 (~~Gossypium hirsutum~~); AI731115 (~~Gossypium hirsutum~~); AI729201 (~~Gossypium hirsutum~~); AI728436 (~~Gossypium hirsutum~~); AI727966 (~~Gossypium hirsutum~~); AI726092 (~~Gossypium hirsutum~~); U73588 (~~Gossypium hirsutum~~); U73587 (~~Gossypium hirsutum~~); AJ012080 (~~Pisum sativum~~); AJ131964 (~~Medicago truncatula~~); AJ131943 (~~Medicago truncatula~~); AJ133726 (~~Lotus japonicus~~); Y16091 (~~Daucus~~

~~carota~~); Y16090 (~~Daucus carota~~); AJ011319 (~~Lycopersicon esculentum~~); AI496671 (~~Glycine max~~); AI496540 (~~Glycine max~~); AI496532 (~~Glycine max~~); AI495774 (~~Glycine max~~); AI495135 (~~Glycine max~~); AI495023 (~~Glycine max~~); AI494833 (~~Glycine max~~); AJ011534 (~~Lycopersicon esculentum~~); Y15802 (~~Hordeum vulgare~~); AI461126 (~~Glycine max~~); AI460757 (~~Glycine max~~); AI460629 (~~Glycine max~~); AI444096 (~~Glycine max~~); AI444083 (~~Glycine max~~); AI444054 (~~Glycine max~~); AI443620 (~~Glycine max~~); AI443476 (~~Glycine max~~); AI443231 (~~Glycine max~~); AI442789 (~~Glycine max~~); AI442411 (~~Glycine max~~); AI441989 (~~Glycine max~~); AI441004 (~~Glycine max~~); AI437923 (~~Glycine max~~); AI437907 (~~Glycine max~~); AI437840 (~~Glycine max~~); AJ010639 (~~Anabaena sp.~~); AJ011535 (~~Lycopersicon esculentum~~); D10266 (~~Vigna radiata~~); L03366 (~~Oryza sativa~~); AF030231 (~~Glycine max~~); M97551 (~~Vicia faba~~); AJ000153 (~~Triticum aestivum~~); AF079523 (~~Musa acuminata~~); AF079851 (~~Pisum sativum~~); AJ001071 (~~Pisum sativum~~); AF049487 (~~Medicago sativa~~); AF054446 (~~Mesembryanthemum crystallinum~~); AA753339 (~~Oryza sativa~~); AA752298 (~~Oryza sativa~~); AA752293 (~~Oryza sativa~~); AA753445 (~~Oryza sativa~~); AA753437 (~~Oryza sativa~~); AA753297 (~~Oryza sativa~~); AA752123 (~~Oryza sativa~~); AA751990 (~~Oryza sativa~~); AA750692 (~~Oryza sativa~~); AA750079 (~~Oryza sativa~~); AA749692 (~~Oryza sativa~~); AA749554 (~~Oryza sativa~~); AA720478 (~~Mesembryanthemum crystallinum~~); AA661050 (~~Medicago truncatula~~); AA661041 (~~Medicago truncatula~~); AA660686 (~~Medicago truncatula~~); D88412 (~~Cotton~~); D10418 (~~Rice~~); D21308 (~~Rice~~); D29733 (~~Rice~~); X81974 (~~B. vulgaris~~); X92378 (~~A. glutinosa~~); Z56278 (~~V. faba~~); Z48640 (~~V. faba~~); X98598 (~~P. sativum~~); T25261 (~~Zea mays~~); T23326 (~~Zea mays~~); T14713 (~~Zea mays~~); T14662 (~~Zea mays~~); T14661 (~~Zea mays~~); X75332 (~~D. carota~~); X02382 (~~Zea mays~~); X02400 (~~Zea mays~~); X70990 (~~A. thaliana~~);

~~X60987 (*A. thaliana*); X69773 (*V. faba*); X73477 (*S. tuberosum*); Z11532 (*S. officinarum*); Z15028 (*O. sativa*); X64770 (*O. sativa*); X59046 (*O. sativa*); X66728 (*H. vulgare*); X65871 (*H. vulgare*); X69931 (*H. vulgare*); A27685 (*O. sativa*); W21612 (*Zea mays*); U24088 (*Solanum tuberosum*); U24087 (*Solanum tuberosum*); X73221 (*H. vulgare*); L32898 (*Zea mays*); F13913 (*Arabidopsis thaliana*); F13912 (*Arabidopsis thaliana*); U21129 (*Solanum tuberosum*); M26672 (*Triticum aestivum*); M26671 (*Triticum aestivum*); L19762 (*Lycopersicon esculentum*); M18745 (*Potato*); L33244 (*Zea mays*); L22296 (*Zea mays*); and Z17959 (*Arabidopsis thaliana*).~~

Claim 17. (Previously presented) The fiber-producing plant according to claim 15, wherein said sucrose synthase gene comprises a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID No 2.

Claim 18. (Withdrawn) A fiber-producing plant according to claim 15, wherein said RNA is capable of reducing an endogenous sucrose synthase gene and said fiber cells have a reduced sucrose synthase activity compared to fiber cells of plant cells which do not comprise said chimeric DNA.

Claim 19. (Withdrawn) The fiber-producing plant according to claim 18, wherein said coding region comprises a nucleotide sequence selected from the group consisting of

a nucleotide sequence comprising at least 19 or 25 contiguous nucleotides having at least 70% sequence identity to a nucleotide sequence

encoding a polypeptide comprising the amino acid sequence of SEQ ID No 2 or the complement thereof; and

a nucleotide sequence comprising at least 19 or 25 contiguous nucleotides having at least 70% sequence identity to a nucleotide sequence encoding a polypeptide comprising the nucleotide sequence of SEQ ID No 1 or the complement thereof.

Claim 20. (Withdrawn) The fiber-producing plant according to claim 18, wherein said coding region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 2208 to the nucleotide at position 2598 or the complement thereof.

Claim 21. (Previously presented) The fiber-producing plant according to any one of claims 15, 16, or 17, wherein said plant is a cotton plant.

Claim 22. (Previously presented) Seeds of a plant according to any one of claims 15, 16, or 17.

Claim 23. (Original) Seeds of a plant according to claim 21.

Claim 24. (Previously presented) Fibers with altered development or properties, isolated from plants according to any one of claims 15, 16, or 17.

Claim 25. (Original) Fibers with altered development or properties, isolated from plants according to claim 21.

Claim 26. (Previously presented) Plants obtained through the methods of any one of claims 1, 2, or 3.

Claim 27. (Original) Plants obtained through the methods of claim 8.

Claim 28. (Original) Plants obtained through the methods of claim 9.

Claim 29. (Original) Plants obtained through the methods claim 10.

Claim 30. (Previously presented) Plants obtained through the methods of any one of claims 12, 13, or 14.